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0500

TEAM 8

RAW SEQUENCE LISTING
PATENT APPLICATION US/08/856,653

DATE: 07/18/97
TIME: 06:15:17

INPUT SET: S19057.raw

> This Raw Listing contains the General
> Information Section and up to the first 5 pages.

```
 1                              SEQUENCE LISTING         ENTERED
 2
 3    (1)     General Information
 4
 5            (i) APPLICANT: Russell, John
 6                           Colpitts, Tracey
 7
 8            (ii) TITLE OF THE INVENTION: REAGENTS AND METHODS USEFUL
 9                      FOR DETECTING DISEASES OF THE PROSTATE
10
11            (iii) NUMBER OF SEQUENCES: 16
12
13            (iv) CORRESPONDENCE ADDRESS:                RECEIVED
14                (A) ADDRESSEE: Abbott Laboratories
15                (B) STREET: 100 Abbott Park Road        FEB    1998
16                (C) CITY: Abbott Park
17                (D) STATE: IL                           GROUP 1800
18                (E) COUNTRY: USA
19                (F) ZIP: 60064-3500
20
21            (v) COMPUTER READABLE FORM:
22                (A) MEDIUM TYPE: Diskette
23                (B) COMPUTER: IBM Compatible
24                (C) OPERATING SYSTEM: DOS
25                (D) SOFTWARE: FastSEQ for Windows Version 2.0
26
27            (vi) CURRENT APPLICATION DATA:
28                (A) APPLICATION NUMBER:
29                (B) FILING DATE:
30                (C) CLASSIFICATION:
31
32            (vii) PRIOR APPLICATION DATA:
33                (A) APPLICATION NUMBER:
34                (B) FILING DATE:
35
36
37
38            (viii) ATTORNEY/AGENT INFORMATION:
39                (A) NAME: Becker, Cheryl L.
40                (B) REGISTRATION NUMBER: 35,441
41                (C) REFERENCE/DOCKET NUMBER: 6105.US.01
42
43            (ix) TELECOMMUNICATION INFORMATION:
44                (A) TELEPHONE: 847/937-6100
45                (B) TELEFAX: 847/938-2623
46                (C) TELEX:
```

```
47
48          (2) INFORMATION FOR SEQ ID NO:1:
49
50          (i) SEQUENCE CHARACTERISTICS:
51              (A) LENGTH: 279 base pairs
52              (B) TYPE: nucleic acid
53              (C) STRANDEDNESS: single
54              (D) TOPOLOGY: linear
55
56
57          (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:
58
59  CAGTGACCAT GAAGGCTGTG CTGCTTGCCC TGTTGATGGC AGGCTTGGCC CTGCAGCCAG     60
60  GCACTGCCCT GCTGTGCTAC TCCTGCAAAG CCCAGGTGAG CAACGAGGAC TGCCTGCAGG    120
61  TGGAGAACTG CACCCAGCTG GGGGAGCAGT GCTGGACCGC GCGCATCCGC GCAGTTGGCC    180
62  TCCTGACCGT CATCAGCAAA GGCTGCAGCT TGAACTGCGT GGATGACTCA CAGGACTACT    240
63  ACGTGGGCAA GAAGAACATC ACGTGCTGTG ACACCGACT                           279
64
65          (2) INFORMATION FOR SEQ ID NO:2:
66
67          (i) SEQUENCE CHARACTERISTICS:
68              (A) LENGTH: 207 base pairs
69              (B) TYPE: nucleic acid
70              (C) STRANDEDNESS: single
71              (D) TOPOLOGY: linear
72
73
74          (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:
75
76  GTGACCATGA AGGCTGTGCT GCTTGCCCTG TTGATGGCAG GCTTGGCCCT GCAGCCAGGC     60
77  ACTGCCCTGC TGTGCTACTC CTGCAAAGCC CAGGTGAGCA ACGAGGACTG CCTGCAGGTG    120
78  GAGAACTGCA CCCAGCTGGG GGAGCAGTGC TGGACCGCGC GCATCCGCGC AGTTGGCCTC    180
79  CTGACCGTCA TCAGCAAAGG CTGCAGC                                        207
80
81          (2) INFORMATION FOR SEQ ID NO:3:
82
83          (i) SEQUENCE CHARACTERISTICS:
84              (A) LENGTH: 265 base pairs
85              (B) TYPE: nucleic acid
86              (C) STRANDEDNESS: single
87              (D) TOPOLOGY: linear
88
89
90          (xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:
91
92  CGAGGACTGC CTGCAGGTGG AGAACTGCAC CCAGCTGGGG GAGCAGTGCT GGACCGCGCG     60
93  CATCCGCGCA GTTGGCCTCC TGACCGTCAT CAGCAAAGGC TGCAGCTTGA ACTGCGTGGA    120
94  TGACTCACAG GACTACTACG TGGGCAAGAA GAACATCACG TGCTGTGACA CCGACTTGTG    180
95  CAACGCCAGC GGGGCCCATG CCCTGCAGCC GGCTGCCGCC ATCCTTGCGC TGCTCCCTGC    240
96  ACTCGGCCTG CTGCTCTGGG GACCC                                          265
97
98          (2) INFORMATION FOR SEQ ID NO:4:
99
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100              (i) SEQUENCE CHARACTERISTICS:
101                  (A) LENGTH: 196 base pairs
102                  (B) TYPE: nucleic acid
103                  (C) STRANDEDNESS: single
104                  (D) TOPOLOGY: linear
105
106
107             (xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:
108
109     CTCGGCCTGC TGCTCTGGGG ACCCGGCCAG CTATAGGCTC TGGGGGGCCC CGCTGCAGCC     60
110     CACACTGGGT GTGGTGCCCC AGGCCTCTGT GCCACTCCTC ACAGACCTGG CCCAGTGGGA    120
111     GCCTGTCCTG GTTCCTGAGG CACATCCTAA CGCAAGTCTG ACCATGTATG TCTGCACCCC    180
112     TGTNCCCCAC CCTGAC                                                     196
113
114              (2) INFORMATION FOR SEQ ID NO:5:
115
116              (i) SEQUENCE CHARACTERISTICS:
117                  (A) LENGTH: 233 base pairs
118                  (B) TYPE: nucleic acid
119                  (C) STRANDEDNESS: single
120                  (D) TOPOLOGY: linear
121
122
123             (xi) SEQUENCE DESCRIPTION: SEQ ID NO:5:
124
125     CTGGCCCAGT GGGAGCCTGT CCTGGTTCCT GAGGCACATC CTAACGCAAG TCTGACCATG     60
126     TATGTCTGCN CCCCTGTCCC CCACCCTGAC CCTCCCATGG CCCTCTCCAG GACTCCCACC    120
127     CGGCAGATCA GCTCTAGTGA CACAGATCCG CCTGCAGATG GCCCCTCCAA CCCTCTCTGC    180
128     TGCTGTTTCC ATGGCCCAGC ATTCTCCACC CTTAACCCTG TGCTCAGGCA CCT           233
129
130              (2) INFORMATION FOR SEQ ID NO:6:
131
132              (i) SEQUENCE CHARACTERISTICS:
133                  (A) LENGTH: 236 base pairs
134                  (B) TYPE: nucleic acid
135                  (C) STRANDEDNESS: single
136                  (D) TOPOLOGY: linear
137
138
139             (xi) SEQUENCE DESCRIPTION: SEQ ID NO:6:
140
141     CCCAGCATTC TCCACCCTTA ACCCTGTGCT CAGGCACCTC TTCCCCCAGG AAGCCTTCCC     60
142     TGCCCACCCC ATCTATGACT TGAGCCAGGT CTGGTCCGTG GTGTCCCCCG CACCCAGCAG    120
143     GGGACAGGCA CTCAGGAGGG CCCAGTAAAG GCTGAGATGA AGTGGACTGA GTAGAACTGG    180
144     AGGACAAGAG TCGACGTGAG TTCCTGGGAG TCTCCAGAGA TGGGGCCTGG AGGCCT         236
145
146              (2) INFORMATION FOR SEQ ID NO:7:
147
148              (i) SEQUENCE CHARACTERISTICS:
149                  (A) LENGTH: 122 base pairs
150                  (B) TYPE: nucleic acid
151                  (C) STRANDEDNESS: single
152                  (D) TOPOLOGY: linear
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INPUT SET: S19057.raw

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153
154
155             (xi) SEQUENCE DESCRIPTION: SEQ ID NO:7:
156
157     CCTGGGAGTC TCCAGAGATG GGGCCTGGAG GCCTGGAGGA ANGGNANCAG GCCTCACATT      60
158     CGTGGGGCTC CCTGAATGGC AGCCTGAGCA CAGCGTAGGC CCTTAATAAA CACCTGTTGG     120
159     AT                                                                   122
160
161             (2) INFORMATION FOR SEQ ID NO:8:
162
163             (i) SEQUENCE CHARACTERISTICS:
164                 (A) LENGTH: 968 base pairs
165                 (B) TYPE: nucleic acid
166                 (C) STRANDEDNESS: single
167                 (D) TOPOLOGY: linear
168
169
170             (xi) SEQUENCE DESCRIPTION: SEQ ID NO:8:
171
172     CAGTGACCAT GAAGGCTGTG CTGCTTGCCC TGTTGATGGC AGGCTTGGCC CTGCAGCCAG      60
173     GCACTGCCCT GCTGTGCTAC TCCTGCAAAG CCCAGGTGAG CAACGAGGAC TGCCTGCAGG     120
174     TGGAGAACTG CACCCAGCTG GGGGAGCAGT GCTGGACCGC GCGCATCCGC GCAGTTGGCC     180
175     TCCTGACCGT CATCAGCAAA GGCTGCAGCT TGAACTGCGT GGATGACTCA CAGGACTACT     240
176     ACGTGGGCAA GAAGAACATC ACGTGCTGTG ACACCGACTT GTGCAACGCC AGCGGGGCCC     300
177     ATGCCCTGCA GCCGGCTGCC GCCATCCTTG CGCTGCTCCC TGCACTCGGC CTGCTGCTCT     360
178     GGGGACCCGG CCAGCTATAG GCTCTGGGGG GCCCCGCTGC AGCCCACACT GGGTGTGGTG     420
179     CCCCAGGCCT CTGTGCCACT CCTCACAGAC CTGGCCCAGT GGGAGCCTGT CCTGGTTCCT     480
180     GAGGCACATC CTAACGCAAG TCTGACCATG TATGTCTGCA CCCCTGTCCC CCACCCTGAC     540
181     CCTCCCATGG CCCTCTCCAG GACTCCCACC CGGCAGATCA GCTCTAGTGA CACAGATCCG     600
182     CCTGCAGATG GCCCCTCCAA CCCTCTCTGC TGCTGTTTCC ATGGCCCAGC ATTCTCCACC     660
183     CTTAACCCTG TGCTCAGGCA CCTCTTCCCC CAGGAAGCCT TCCCTGCCCA CCCCATCTAT     720
184     GACTTGAGCC AGGTCTGGTC CGTGGTGTCC CCCGCACCCA GCAGGGGACA GGCACTCAGG     780
185     AGGGCCCAGT AAAGGCTGAG ATGAAGTGGA CTGAGTAGAA CTGGAGGACA AGAGTCGACG     840
186     TGAGTTCCTG GGAGTCTCCA GAGATGGGGC CTGGAGGCCT GGAGGAANGG NANCAGGCCT     900
187     CACATTCGTG GGGCTCCCTG AATGGCAGCC TGAGCACAGC GTAGGCCCTT AATAAACACC     960
188     TGTTGGAT                                                             968
189
190             (2) INFORMATION FOR SEQ ID NO:9:
191
192             (i) SEQUENCE CHARACTERISTICS:
193                 (A) LENGTH: 68 base pairs
194                 (B) TYPE: nucleic acid
195                 (C) STRANDEDNESS: single
196                 (D) TOPOLOGY: linear
197
198             (xi) SEQUENCE DESCRIPTION: SEQ ID NO:9:
199
200     AGCTCGGAAT TCCGAGCTTG GATCCTCTAG AGCGGCCGCC GACTAGTGAG CTCGTCGACC      60
201     CGGGAATT                                                              68
202
203             (2) INFORMATION FOR SEQ ID NO:10:
204
205             (i) SEQUENCE CHARACTERISTICS:
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206                 (A) LENGTH: 68 base pairs
207                 (B) TYPE: nucleic acid
208                 (C) STRANDEDNESS: single
209                 (D) TOPOLOGY: linear
210
211
212          (xi) SEQUENCE DESCRIPTION: SEQ ID NO:10:
213
214     AATTAATTCC CGGGTCGACG AGCTCACTAG TCGGCGGCCG CTCTAGAGGA TCCAAGCTCG        60
215     GAATTCCG                                                                 68
216
217              (2) INFORMATION FOR SEQ ID NO:11:
218
219              (i) SEQUENCE CHARACTERISTICS:
220                  (A) LENGTH: 123 amino acids
221                  (B) TYPE: amino acid
222                  (C) STRANDEDNESS: single
223                  (D) TOPOLOGY: linear
224
225              (ii) MOLECULE TYPE: None
226
227              (xi) SEQUENCE DESCRIPTION: SEQ ID NO:11:
228
229     Met Lys Ala Val Leu Leu Ala Leu Leu Met Ala Gly Leu Ala Leu Gln
230      1               5                   10                  15
231     Pro Gly Thr Ala Leu Leu Cys Tyr Ser Cys Lys Ala Gln Val Ser Asn
232                 20                  25                  30
233     Glu Asp Cys Leu Gln Val Glu Asn Cys Thr Gln Leu Gly Glu Gln Cys
234             35                  40                  45
235     Trp Thr Ala Arg Ile Arg Ala Val Gly Leu Leu Thr Val Ile Ser Lys
236          50                  55                  60
237     Gly Cys Ser Leu Asn Cys Val Asp Asp Ser Gln Asp Tyr Tyr Val Gly
238     65                  70                  75                  80
239     Lys Lys Asn Ile Thr Cys Cys Asp Thr Asp Leu Cys Asn Ala Ser Gly
240                     85                  90                  95
241     Ala His Ala Leu Gln Pro Ala Ala Ala Ile Leu Ala Leu Leu Pro Ala
242                 100                 105                 110
243     Leu Gly Leu Leu Leu Trp Gly Pro Gly Gln Leu
244             115                 120
245
246              (2) INFORMATION FOR SEQ ID NO:12:
247
248              (i) SEQUENCE CHARACTERISTICS:
249                  (A) LENGTH: 34 amino acids
250                  (B) TYPE: amino acid
251                  (C) STRANDEDNESS: single
252                  (D) TOPOLOGY: linear
253
254              (ii) MOLECULE TYPE: None
255
256              (xi) SEQUENCE DESCRIPTION: SEQ ID NO:12:
257
258     Thr Ala Leu Leu Cys Tyr Ser Cys Lys Ala Gln Val Ser Asn Glu Asp
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SEQUENCE VERIFICATION REPORT
PATENT APPLICATION   *US/08/856,653*

INPUT SET: S19057.raw

Line	Error	Original Text